

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number:

10/ S18,184

Source:

PCF

Date Processed by STIC:

12-28-04

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/518,184

TIME: 11:53:52

Input Set : A:\3057US0P.SEQ.txt

Output Set: N:\CRF4\12282004\J518184.raw

```

3 <110> APPLICANT: WATANABE, TATSUYA
4   INAZUKA, MASAKAZU
6 <120> TITLE OF INVENTION: Prophylactic/therapeutic agents for bone or joint diseases
8 <130> FILE REFERENCE: 3057 USOP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/518,184
C--> 11 <141> CURRENT FILING DATE: 2004-12-16
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/007741
W--> 14 <151> PRIOR FILING DATE: 2003-6-18
16 <150> PRIOR APPLICATION NUMBER: JP2002-178715
W--> 17 <151> PRIOR FILING DATE: 2002-6-19
19 <160> NUMBER OF SEQ ID NOS: 6
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 871
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
27 Met Lys Tyr Ser Cys Cys Ala Leu Val Leu Ala Val Leu Gly Thr Glu
28           5                      10                      15
29 Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
30           20                      25                      30
31 Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
32           35                      40                      45
33 Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
34           50                      55                      60
35 Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
36 65           70                      75                      80
37 Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
38           85                      90                      95
39 Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
40           100                     105                     110
41 Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
42           115                     120                     125
43 Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
44           130                     135                     140
45 Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
46 145           150                     155                     160
47 Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
48           165                     170                     175
49 Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
50           180                     185                     190
51 Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
52           195                     200                     205
53 Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro

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54      210      215      220
55 His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
56 225      230      235      240
57 Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
58      245      250      255
59 Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
60      260      265      270
61 Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
62      275      280      285
63 Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
64      290      295      300
65 Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
66 305      310      315      320
67 Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
68      325      330      335
69 Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
70      340      345      350
71 Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
72      355      360      365
73 Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
74      370      375      380
75 Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
76 385      390      395      400
77 Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
78      405      410      415
79 Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
80      420      425      430
81 Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
82      435      440      445
83 Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
84      450      455      460
85 Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
86 465      470      475      480
87 Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
88      485      490      495
89 Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
90      500      505      510
91 Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
92      515      520      525
93 Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
94      530      535      540
95 Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
96 545      550      555      560
97 Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
98      565      570      575
99 His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
100      580      585      590
101 Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
102      595      600      605

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103 Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
104      610                               615                      620
105 Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
106 625                               630                      635                      640
107 Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
108                               645                      650                      655
109 Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
110                               660                      665                      670
111 Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
112                               675                      680                      685
113 Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
114      690                               695                      700
115 Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
116 705                               710                      715                      720
117 Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
118                               725                      730                      735
119 Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
120                               740                      745                      750
121 His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
122                               755                      760                      765
123 Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
124      770                               775                      780
125 Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
126 785                               790                      795                      800
127 Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
128                               805                      810                      815
129 Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
130                               820                      825                      830
131 Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
132                               835                      840                      845
133 Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
134      850                               855                      860
135 Leu Trp Asp Gly Trp Glu Gly
136 865                               870
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 2613
140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 2
144 atgaagtatt cttgctgtgc tctgggttttg gctgtcctgg gcacagaatt gctgggaagc      60
145 ctctgttcga ctgtcagatc cccgagggttc agaggacgga tacagcagga acgaaaaaac      120
146 atccgaccca acattattct tgtgcttacc gatgatcaag atgtggagct ggggtccctg      180
147 caagtcatga acaaaacgag aaagattatg gaacatgggg gggccacctt catcaatgcc      240
148 tttgtgacta caccatgtg ctgcccgtca cggctctcca tgctcaccgg gaagtatgtg      300
149 cacaatcaca atgtctacac caacaacgag aactgctctt cccctcgtg gcaggccatg      360
150 catgagcctc ggacttttgc tgtatatctt aacaacactg gctacagaac agcctttttt      420
151 ggaaaatacc tcaatgaata taatggcagc tacatcccc ctgggtggcg agaattggctt      480
152 ggattaatca agaattctcg cttctataat tacactgttt gtcgcaatgg catcaaagaa      540
153 aagcatggat ttgattatgc aaaggactac ttcacagact taatcactaa cgagagcatt      600

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154 aattactttca aaatgtctaa gagaatgtat ccccatagggc ccgttatgat ggtgatcagc 660
155 cacgctgctc cccacggccc cgaggactca gccccacagt tttctaaact gtaccccaat 720
156 gcttcccaac acataactcc tagttataac tatgcaccaa atatggataa acactggatt 780
157 atgcagtaca caggaccaat gctgcccac cccatggaat ttacaaacat tctacagcgc 840
158 aaaaggctcc agactttgat gtcagtggat gattctgtgg agaggctgta taacatgctc 900
159 gtggagacgg gggagctgga gaatacttac atcatttaca ccgccgacca tggttaccat 960
160 attgggcagt ttggactggg caaggggaaa tccatgccat atgactttga tattcgtgtg 1020
161 ccttttttta ttcgtggtcc aagtgtagaa ccaggatcaa tagtcccaca gatcgttctc 1080
162 aacattgact tggcccccac gatcctggat attgctgggc tcgacacacc tctgatgtg 1140
163 gacggcaagt ctgtcctcaa acttctggac ccagaaaagc caggtaacag gtttcgaaca 1200
164 aacaagaagg ccaaaatttg gcgtgataca ttcctagtgg aaagaggcaa atttctacgt 1260
165 aagaaggaa aatccagcaa gaatatccaa cagtcaaact acttgcccaa atatgaacgg 1320
166 gtcaaagaac tatgccagca ggccaggtag cagacagcct gtgaacaacc ggggcagaag 1380
167 tggcaatgca ttgaggatac atctggcaag cttcgaattc acaagtgtaa aggacccagt 1440
168 gacctgctca cagtccggca gagcacgcgg aacctctacg ctccgggctt ccatgacaaa 1500
169 gacaaaagat gcagttgtag ggagtctggg taccgtgcca gcagaagcca aagaaagagt 1560
170 caacggcaat tcttgagaaa ccaggggact ccaaagtaca agcccagatt tgtccatact 1620
171 cggcagacac gttccttgct cgtcgaattt gaaggtgaaa tatatgacat aaatctggaa 1680
172 gaagaagaag aattgcaagt gttgcaacca agaaacattg ctaagcgtca tgatgaaggc 1740
173 cacaaggggc caagagatct ccaggcttcc agtgggtggc acaggggcag gatgctggca 1800
174 gatagcagca acgcccgtggg cccacctacc actgtccgag tgacacacaa gtgttttatt 1860
175 cttcccaatg actctatcca ttgtgagaga gaactgtacc aatcgggccag agcgtggaag 1920
176 gaccataagg catacattga caaagagatt gaagctctgc aagataaaaat taagaattta 1980
177 agagaagtga gaggacatct gaagagaagg aagcctgagg aatgtagctg cagtaaacaa 2040
178 agctattaca ataaagagaa aggtgtaaaa aagcaagaga aattaaagag ccatcttcac 2100
179 ccattcaagg aggctgctca ggaagtagat agcaaactgc aacttttcaa ggagaacaac 2160
180 cgtaggagga agaaggagag gaaggagaag agacggcaga ggaaggggga agagtgcagc 2220
181 ctgcctggcc tcaattgctt cacgcagtac aacaaccact ggcagacagc cccgttctgg 2280
182 aacctgggat ctttctgtgc ttgcacgagt tctaacaata acacctactg gtgtttgcgt 2340
183 acagttaatg agacgcataa ttttcttttc tgtgagtttg ctactggctt tttggagtat 2400
184 tttgatatga atacagatcc ttatcagctc acaataacag tgcacacggg agaacgaggc 2460
185 attttgaatc agctacacgt acaactaatg gagctcagaa gctgtcaagg atataagcag 2520
186 tgcaacccaa gacctaagaa tcttgatgtt ggaaataaag atggaggaag ctatgacct 2580
187 cacagaggac agttatggga tggatgggaa ggt 2613

```

189 <210> SEQ ID NO: 3

190 <211> LENGTH: 39

191 <212> TYPE: DNA

192 <213> ORGANISM: Artificial Sequence

194 <220> FEATURE:

195 <223> OTHER INFORMATION: Primer

197 <400> SEQUENCE: 3

198 tggaccaa acaatgaagt attcttgctg tgctctggg

39

200 <210> SEQ ID NO: 4

201 <211> LENGTH: 31

202 <212> TYPE: DNA

203 <213> ORGANISM: Artificial Sequence

205 <220> FEATURE:

206 <223> OTHER INFORMATION: Primer

208 <400> SEQUENCE: 4

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209 ggcaagggtca aatgaggtgt tttcccaacc t 31
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Primer
219 <400> SEQUENCE: 5
220 gagagaggcg aatggaacga 20
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 19
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Primer
W--> 229 <400> SEQUENCE: 6
230 cgcaccaggg agctgatct 19
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VERIFICATION SUMMARY

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Input Set : A:\3057USOP.SEQ.txt

Output Set: N:\CRF4\12282004\J518184.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:229 M:283 W: Missing Blank Line separator, <400> field identifier